

09/980862

JC10 Rec'd PCT/PTC 07 DEC 2001

1

SEQUENCE LISTINGS

<110> Skerra, Arne, Prof. Dr.

5 <120> Muteins of bilin-binding protein

<150> DE 199 26 068.0

<151> 1999-06-08

10 <160> 18

<210> 1

<211> 1219 base pairs

<212> DNA

15 <213> artificial sequence

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<221> sig_peptide

<222> (22)...(84)

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<221> mat_peptide

<222> (85)...(1209)

<223> fusion protein of bilin-binding protein, Strep-tag II und fragment

25 of phage coat protein pIII

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<221> CDS

<222> (85)...(606)

30 <223> mature bilin-binding protein

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<222> (607)...(636)

35 <223> Strep-tag II-affinity tag

<220>

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<223> amber stop codon

 $\langle 220 \rangle$

5 <221> CDS

 $\langle 222 \rangle \quad (640) \dots (1209)$

<223> amino acids 217-406 of coat protein pIII

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	Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe															
	5 10 15															
25	GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC 180															
	Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr															
	20 25 30															
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	Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr															
	35 40 45															
35	ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC 270															
	Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile															
	50 55 60															
40	CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT 315															
	His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly															
	65 70 75															
45	GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT 360															
	Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly															
	80 85 90															
50	GTC ACC AAG GAG AAC GTA TTC AAC GTA CTC TCC ACT GAC AAC AAG 405															
	Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys															
	95 100 105															
55	AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG 450															
	Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys															
	110 115 120															
60	GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT 495															
	Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu															
	125 130 135															

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			140					145					150			
5	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
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	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
15	GAA	AAA	TAG	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGC	GGC	GGC	675
	Glu	Lys	Gln	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
			185					190					195			
20	TCT	GAG	GGT	GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	720
	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	
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25	TCT	GAG	GGA	GGC	GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	765
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			215					220					225			
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35	AAT	GCC	GAT	GAA	AAC	GCG	CTA	CAG	TCT	GAC	GCT	AAA	GGC	AAA	CTT	855
	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	Lys	Gly	Lys	Leu	
			245					250					255			
40	GAT	TCT	GTC	GCT	ACT	GAT	TAC	GGT	GCT	GCT	ATC	GAT	GGT	TTC	ATT	900
	Asp	Ser	Val	Ala	Thr	Asp	Tyr	Gly	Ala	Ala	Ile	Asp	Gly	Phe	Ile	
			260					265					270			
45	GGT	GAC	GTT	TCC	GGC	CTT	GCT	AAT	GGT	AAT	GGT	GCT	ACT	GGT	GAT	945
	Gly	Asp	Val	Ser	Gly	Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	Gly	Asp	
			275					280					285			
50	TTT	GCT	GGC	TCT	AAT	TCC	CAA	ATG	GCT	CAA	GTC	GGT	GAC	GGT	GAT	990
	Phe	Ala	Gly	Ser	Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	Asp	
			290					295					300			
55	AAT	TCA	CCT	TTA	ATG	AAT	AAT	TTC	CGT	CAA	TAT	TTA	CCT	TCC	CTC	1035
	Asn	Ser	Pro	Leu	Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	
			305					310					315			
60	CCT	CAA	TCG	GTT	GAA	TGT	CGC	CCT	TTT	GTC	TTT	GGC	GCT	GGT	AAA	1080
	Pro	Gln	Ser	Val	Glu	Cys	Arg	Pro	Phe	Val	Phe	Gly	Ala	Gly	Lys	
			320					325					330			
65	CCA	TAT	GAA	TTT	TCT	ATT	GAT	TGT	GAC	AAA	ATA	AAC	TTA	TTC	CGT	1125
	Pro	Tyr	Glu	Phe	Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	
			335					340					345			
70	GGT	GTC	TTT	GCG	TTT	CTT	TTA	TAT	GTT	GCC	ACC	TTT	ATG	TAT	GTA	1170
	Gly	Val	Phe	Ala	Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	
			350					355					360			

TTT TCT ACG TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT 1209
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10 <212> DNA

<213> artificial sequence

<220>

<223> primer

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<210> 4

<211> 74 bases

<212> DNA

<213> artificial sequence

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<220>

<223> primer

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<400> 5

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ASNNGCAMNN GTATCCGATG ATGTAAGTT 78

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<223> primer

<400> 6

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CTTCGACTGG TCCCAGTACC ATGGTAAATG GTGGGA 36

<210> 7

35 <211> 37 bases

<212> DNA

<213> artificial sequence

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<223> mature bilin-binding protein

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Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys
110 115 120

GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT 495
 Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu
 125 130 135

5 ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC GGC TCC 540
 Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser
 140 145 150

10 CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC TCT GAA 585
 Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu
 155 160 165

15 GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT CAC CCG CAG TTC 630
 Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe
 170 175 180

GAA AAA CCA GCT AGC CTG GCT GAA GCT AAA GTT CTG GCT AAC CGT 675
 Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg
 185 190 195

20 GAA CTG GAC AAA TAC GGT GTT TCC GAC TAC TAC AAA AAC CTC ATC 720
 Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile
 200 205 210

25 AAC AAC GCT AAA ACC GTT GAA GGT GTT AAA GCT CTG ATC GAC GAA 765
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45 <210> 11

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<400> 11

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GACTACTGGG GAGCCGA 17

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<220>

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1				5					10					15	

25

AAC	TTC	GAC	TGG	TCC	CAG	TAC	CAT	GGT	AAA	TGG	TGG	GAA	GTC	GCC	90
Asn	Phe	Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	Glu	Val	Ala	
				20					25					30	

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AAA	TAC	CCC	CAT	CAC	GAG	CGG	AAG	TAC	GGA	AAG	TGC	GGA	TGG	GCT	135
Lys	Tyr	Pro	His	His	Glu	Arg	Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	
				35					40					45	

35

GAG	TAC	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	CGC	TAC	TCT	180
Glu	Tyr	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Arg	Tyr	Ser	
				50					55					60	

40

GTA	ATC	CAC	GGC	AAG	GAA	TAC	TTT	TCC	GAA	GGT	ACC	GCC	TAC	CCA	225
Val	Ile	His	Gly	Lys	Glu	Tyr	Phe	Ser	Glu	Gly	Thr	Ala	Tyr	Pro	
				65					70					75	

45

GTT	GGT	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	TAC	ACT	ATT	270
Val	Gly	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Tyr	Thr	Ile	
				80					85					90	

45

GGA	GGT	GTG	ACC	CAG	GAG	GGT	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	315
Gly	Gly	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	
				95					100					105	

10

AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC GAG GAC 360
 Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp
 110 115 120

5 AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA AGC ATG 405
 Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met
 125 130 135

10 GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC 450
 Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile
 140 145 150

15 GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC 495
 Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
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<210> 13

<211> 76 bases

<212> DNA

25 <213> artificial sequence

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<223> primer

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<211> 1219 bases pairs

<212> DNA

<213> fragment of phasmids pBBP24

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<221> sig_peptide

<222> (22)...(84)

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<222> (85)...(1209)

<223> fusion protein of bilin-binding protein, Strep-Tag II and fragment
5 of phage coat protein pIII, with interrupted reading frame

<220>

<221> CDS

<222> (85)...(606)

10 <223> mature bilin-binding protein with interrupted reading frame

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<222> (607)...(636)

15 <223> Strep-Tag II affinity tag

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<222> (637)...(639)

20 <223> amber stop codon

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<222> (640)...(1209)

25 <223> amino acids 217-406 of coat protein pIII

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	-10 -5 -1 1	
40	TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA GTC GAC AAC TTC	135
	Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe	
	5 10 15	
	GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC	180
	Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr	
	20 25 30	

	CCC AAC TCA GTT GAG AAG TAC GGA AAT TAA TGA TGG GCT GAG TAC	225
	Pro Asn Ser Val Glu Lys Tyr Gly Asn Trp Ala Glu Tyr	
	35 40 45	
5	ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC	270
	Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile	
	50 55 60	
10	CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT	315
	His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly	
	65 70 75	
15	GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT	360
	Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly	
	80 85 90	
20	GTC ACC AAG GAG AAC GTA TTC AAC GTA CTC TCC ACT GAC AAC AAG	405
	Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys	
	95 100 105	
	AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG	450
	Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys	
	110 115 120	
25	GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT	495
	Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu	
	125 130 135	
30	ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC GGC TCC	540
	Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser	
	140 145 150	
35	CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC TCT GAA	585
	Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu	
	155 160 165	
40	GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT CAC CCG CAG TTC	630
	Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe	
	170 175 180	
	GAA AAA TAG GCT GGC GGC GGC TCT GGT GGT GGT TCT GGC GGC GGC	675
	Glu Lys Gln Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly	
	185 190 195	
45	TCT GAG GGT GGT GGC TCT GAG GGT GGC GGT TCT GAG GGT GGC GGC	720
	Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly	
	200 205 210	
50	TCT GAG GGA GGC GGT TCC GGT GGT GGC TCT GGT TCC GGT GAT TTT	765
	Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe	
	215 220 225	
55	GAT TAT GAA AAG ATG GCA AAC GCT AAT AAG GGG GCT ATG ACC GAA	810
	Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu	
	230 235 240	
60	AAT GCC GAT GAA AAC GCG CTA CAG TCT GAC GCT AAA GGC AAA CTT	855
	Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu	
	245 250 255	

14

	1	5	10	15	
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5	Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala	30			
		20	25	30	
	GCG TAC CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA TGG GCT	135			
10	Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala	45			
		35	40	45	
	GAG TAC ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG CGC TAC TCT	180			
	Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser	60			
		50	55	60	
15	GTA ATC CAC GGC AAG GAA TAC TTT TCC GAA GGT ACC GCC TAC CCA	225			
	Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro	75			
		65	70	75	
	GTT GGT GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC TAC ACT ATT	270			
20	Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile	90			
		80	85	90	
	GGA GGT GTG ACC CAG GAG GGT GTA TTC AAC GTA CTC TCC ACT GAC	315			
25	Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp	105			
		95	100	105	
	AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC GAG GAC	360			
30	Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp	120			
		110	115	120	
	AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA AGC ATG	405			
	Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met	135			
		125	130	135	
35	GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC	450			
	Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile	150			
		140	145	150	
	GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC	495			
40	Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	165			
		155	160	165	
	TCT GAA GCC GCC TGC AAG GTC AAC AAT	522			
45	Ser Glu Ala Ala Cys Lys Val Asn Asn	170			

<210> 16

<211> 1380 base pairs

50 <212> DNA

<213> fragment of plasmids PBBP21

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<221> sig_peptide

$\langle 222 \rangle \quad (22) \dots (84)$ $\langle 220 \rangle$

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<221> mat_peptide
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5 $\langle 222 \rangle$ (85) ... (636)

<223> fusion protein of bilin-binding protein and Strep-Tag II

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<221> sig_peptide

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<222> (718) ... (1365)

15 <223> DsbC protein

<400> 16

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-21 -20 -15

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Ala Val Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val

25 -10 -5 -1 1

TAC	CAC	GAC	GGT	GCC	TGT	CCC	GAA	GTC	AAG	CCA	GTC	GAC	AAC	TTC	135
Tyr	His	Asp	Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	
		5					10					15			

GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG GAA GTC GCC AAA TAC 180
Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
20 25 30

35 CCC AAC TCA GTT GAG AAG TAC GGA AAG TGC GGA TGG GCT GAG TAC 225
Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr

 35 40 45

ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG AAC TAC CAC GTA ATC 270
Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile

50 55 60

45 CAC GGC AAG GAA TAC TTT ATT GAA GGA ACT GCC TAC CCA GTT GGT 315
His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly
65 70 75

GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC CTG ACT TAC GGA GGT 360
Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly
80 85 90

	GTC ACC AAG GAG AAC GTA TTC AAC GTA CTC TCC ACT GAC AAC AAG	405
	Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys	
	95 100 105	
5	AAC TAC ATC ATC GGA TAC TAC TGC AAA TAC GAC GAG GAC AAG AAG	450
	Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys	
	110 115 120	
10	GGA CAC CAA GAC TTC GTC TGG GTG CTC TCC AGA AGC ATG GTC CTT	495
	Gly His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu	
	125 130 135	
15	ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC CTT ATC GGC TCC	540
	Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser	
	140 145 150	
20	CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT GAC TTC TCT GAA	585
	Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu	
	155 160 165	
	GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT CAC CCG CAG TTC	630
	Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe	
	170 175 180	
25	GAA AAA TAATAAGCTT CGGGAAGATT T ATG AAG AAA GGT TTT ATG	675
	Glu Lys Met Lys Lys Gly Phe Met	
	-20 -15	
30	TTG TTT ACT TTG TTA GCG GCG TTT TCA GGC TTT GCT CAG GCT GAT	720
	Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly Phe Ala Gln Ala Asp	
	-10 -5 -1 1	
35	GAC GCG GCA ATT CAA CAA ACG TTA GCC AAA ATG GGC ATC AAA AGC	765
	Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser	
	5 10 15	
40	AGC GAT ATT CAG CCC GCG CCT GTA GCT GGC ATG AAG ACA GTT CTG	810
	Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu	
	20 25 30	
45	ACT AAC AGC GGC GTG TTG TAC ATC ACC GAT GAT GGT AAA CAT ATC	855
	Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile	
	35 40 45	
	ATT CAG GGG CCA ATG TAT GAC GTT AGT GGC ACG GCT CCG GTC AAT	900
	Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val Asn	
	50 55 60	
50	GTC ACC AAT AAG ATG CTG TTA AAG CAG TTG AAT GCG CTT GAA AAA	945
	Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys	
	65 70 75	
55	GAG ATG ATC GTT TAT AAA GCG CCG CAG GAA AAA CAC GTC ATC ACC	990
	Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr	
	80 85 90	
60	GTG TTT ACT GAT ATT ACC TGT GGT TAC TGC CAC AAA CTG CAT GAG	1035
	Val Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu	
	95 100 105	

CAA ATG GCA GAC TAC AAC GCG CTG GGG ATC ACC GTG CGT TAT CTT 1080
 Gln Met Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu
 110 115 120

5

GCT TTC CCG CGC CAG GGG CTG GAC AGC GAT GCA GAG AAA GAA ATG 1125
 Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met
 125 130 135

10

AAA GCT ATC TGG TGT GCG AAA GAT AAA AAC AAA GCG TTT GAT GAT 1170
 Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp
 140 145 150

15

GTG ATG GCA GGT AAA AGC GTC GCA CCA GCC AGT TGC GAC GTG GAT 1215
 Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys Asp Val Asp
 155 160 165

20

ATT GCC GAC CAT TAC GCA CTT GGC GTC CAG CTT GGC GTT AGC GGT 1260
 Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val Ser Gly
 170 175 180

25

ACT CCG GCA GTT GTG CTG AGC AAT GGC ACA CTT GTT CCG GGT TAC 1305
 Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu Val Pro Gly Tyr
 185 190 195

CAG CCG CCG AAA GAG ATG AAA GAA TTC CTC GAC GAA CAC CAA AAA 1350
 Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys
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ATG ACC AGC GGT AAA TAATTCGCGT AGCTT 1380
 Met Thr Ser Gly Lys
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 <223> fusion protein of alkaline phosphatase, linker peptide Pro-Pro-Ser-
 Ala, mutein DigA16 and Strep-Tag II

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 Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala
 50 55 60

5	CGT	AAT	TAT	GCC	GAA	GGT	GCG	GGC	GGC	TTT	TTT	AAA	GGT	ATA	GAT	316
	Arg	Asn	Tyr	Ala	Glu	Gly	Ala	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	
			65					70					75			
10	GCC	TTA	CCG	CTT	ACC	GGG	CAA	TAC	ACT	CAC	TAT	GCG	CTG	AAT	AAA	361
	Ala	Leu	Pro	Leu	Thr	Gly	Gln	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	
			80					85					90			
15	AAA	ACC	GGC	AAA	CCG	GAC	TAC	GTC	ACC	GAC	TCG	GCT	GCA	TCA	GCA	406
	Lys	Thr	Gly	Lys	Pro	Asp	Tyr	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	
			95					100					105			
20	ACC	GCC	TGG	TCA	ACC	GGT	GTC	AAA	ACC	TAT	AAC	GGC	GCG	CTG	GGC	451
	Thr	Ala	Trp	Ser	Thr	Gly	Val	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	
			110					115					120			
25	GTC	GAT	ATT	CAC	GAA	AAA	GAT	CAC	CCA	ACG	ATT	CTG	GAA	ATG	GCA	496
	Val	Asp	Ile	His	Glu	Lys	Asp	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	
			125					130					135			
30	AAA	GCC	GCA	GGT	CTG	GCG	ACC	GGT	AAC	GTT	TCT	ACC	GCA	GAG	TTG	541
	Lys	Ala	Ala	Gly	Leu	Ala	Thr	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	
			140					145					150			
35	CAG	GAT	GCC	ACG	CCC	GCT	GCG	CTG	GTG	GCA	CAT	GTG	ACC	TCG	CGC	586
	Gln	Asp	Ala	Thr	Pro	Ala	Ala	Leu	Val	Ala	His	Val	Thr	Ser	Arg	
			155					160					165			
40	AAA	TGC	TAC	GGT	CCG	AGC	GCG	ACC	AGT	GAA	AAA	TGT	CCG	GGT	AAC	631
	Lys	Cys	Tyr	Gly	Pro	Ser	Ala	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	
			170					175					180			
45	GCT	CTG	GAA	AAA	GGC	GGA	AAA	GGA	TCG	ATT	ACC	GAA	CAG	CTG	CTT	676
	Ala	Leu	Glu	Lys	Gly	Gly	Lys	Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	
			185					190					195			
50	AAC	GCT	CGT	GCC	GAC	GTT	ACG	CTT	GGC	GGC	GGC	GCA	AAA	ACC	TTT	721
	Asn	Ala	Arg	Ala	Asp	Val	Thr	Leu	Gly	Gly	Gly	Ala	Lys	Thr	Phe	
			200					205					210			
55	GCT	GAA	ACG	GCA	ACC	GCT	GGT	GAA	TGG	CAG	GGA	AAA	ACG	CTG	CGT	766
	Ala	Glu	Thr	Ala	Thr	Ala	Gly	Glu	Trp	Gln	Gly	Lys	Thr	Leu	Arg	
			215					220					225			
60	GAA	CAG	GCA	CAG	GCG	CGT	GGT	TAT	CAG	TTG	GTG	AGC	GAT	GCT	GCC	811
	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	Gln	Leu	Val	Ser	Asp	Ala	Ala	
			230					235					240			
65	TCA	CTG	AAT	TCG	GTG	ACG	GAA	GCG	AAT	CAG	CAA	AAA	CCC	CTG	CTT	856
	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	Asn	Gln	Gln	Lys	Pro	Leu	Leu	
			245					250					255			
70	GGC	CTG	TTT	GCT	GAC	GGC	AAT	ATG	CCA	GTG	CGC	TGG	CTA	GGA	CCG	901
	Gly	Leu	Phe	Ala	Asp	Gly	Asn	Met	Pro	Val	Arg	Trp	Leu	Gly	Pro	
			260					265					270			
75	AAA	GCA	ACG	TAC	CAT	GGC	AAT	ATC	GAT	AAG	CCC	GCA	GTC	ACC	TGT	946
	Lys	Ala	Thr	Tyr	His	Gly	Asn	Ile	Asp	Lys	Pro	Ala	Val	Thr	Cys	
			275					280					285			

	ACG CCA AAT CCG CAA CGT AAT GAC AGT GTA CCA ACC CTG GCG CAG	991
	Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln	
	290 295 300	
5	ATG ACC GAC AAA GCC ATT GAA TTG TTG AGT AAA AAT GAG AAA GGC	1036
	Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly	
	305 310 315	
10	TTT TTC CTG CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT CAT	1081
	Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His	
	320 325 330	
15	GCT GCG AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT CTC GAT	1126
	Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp	
	335 340 345	
20	GAA GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG GAG GGT AAC	1171
	Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn	
	350 355 360	
	ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC CAC GCC AGC CAG ATT	1216
	Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile	
	365 370 375	
25	GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ACC CAG GCG CTA AAT	1261
	Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn	
	380 385 390	
30	ACC AAA GAT GGC GCA GTG ATG GTG ATG AGT TAC GGG AAC TCC GAA	1306
	Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu	
	395 400 405	
35	GAG GAT TCA CAA GAA CAT ACC GGC AGT CAG TTG CGT ATT GCG GCG	1351
	Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala	
	410 415 420	
40	TAT GGC CCG CAT GCC GCC AAT GTT GTT GGA CTG ACC GAC CAG ACC	1396
	Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr	
	425 430 435	
	GAT CTC TTC TAC ACC ATG AAA GCC GCT CTG GGG CTG AAA CCG CCT	1441
	Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro	
	440 445 450	
45	AGC GCT GAC GTG TAC CAC GAC GGT GCC TGT CCC GAA GTC AAG CCA	1486
	Ser Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro	
	455 460 465	
50	GTC GAC AAC TTC GAC TGG TCC CAG TAC CAT GGT AAA TGG TGG CAG	1531
	Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln	
	470 475 480	
55	GTC GCC GCG TAC CCC GAT CAT ATT ACG AAG TAC GGA AAG TGC GGA	1576
	Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly	
	485 490 495	
60	TGG GCT GAG TAC ACT CCT GAA GGC AAG AGT GTC AAA GTT TCG CGC	1621
	Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg	
	500 505 510	

TAC TCT GTA ATC CAC GGC AAG GAA TAC TTT TCC GAA GGT ACC GCC 1666
 Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala
 515 520 525
 5 TAC CCA GTT GGT GAC TCC AAG ATT GGA AAG ATC TAC CAC AGC TAC 1711
 Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr
 530 535 540
 10 ACT ATT GGA GGT GTG ACC CAG GAG GGT GTA TTC AAC GTA CTC TCC 1756
 Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser
 545 550 555
 15 ACT GAC AAC AAG AAC TAC ATC ATC GGA TAC TTT TGC TCG TAC GAC 1801
 Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp
 560 565 570
 20 GAG GAC AAG AAG GGA CAC ATG GAC TTG GTC TGG GTG CTC TCC AGA 1846
 Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg
 575 580 585
 AGC ATG GTC CTT ACT GGT GAA GCC AAG ACC GCT GTC GAG AAC TAC 1891
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr
 590 595 600
 25 CTT ATC GGC TCC CCA GTA GTC GAC TCC CAG AAA CTG GTA TAC AGT 1936
 Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser
 605 610 615
 30 GAC TTC TCT GAA GCC GCC TGC AAG GTC AAC AAT AGC AAC TGG TCT 1981
 Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser
 620 625 630
 35 CAC CCG CAG TTC GAA AAA TAATAAGCTT 2009
 His Pro Gln Phe Glu Lys
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<223> fusion protein of mutein DigA16, Strep-Tag II, linker peptide Gly(5) and alkaline phosphatase

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5 <221> CDS

<222> (85)...(606)

<223> mutein DigA16

<220>

10 <221> CDS

<222> (607)...(636)

<223> Strep-Tag II affinity tag

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<222> (637)...(651)

<223> linker peptide Gly-Gly-Gly-Gly-Gly

<220>

20 <221> CDS

<222> (652)...(1998)

<223> alkaline phosphatase without signalling sequence and N-terminal Arg

<400> 18

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			Met	Lys	Lys	Thr	Ala	Ile	Ala	Ile	
			-21	-20					-15		

30

GCA	GTG	GCA	CTG	GCT	GGT	TTC	GCT	ACC	GTA	GCG	CAG	GCC	GAC	GTG	90
Ala	Val	Ala	Leu	Ala	Gly	Phe	Ala	Thr	Val	Ala	Gln	Ala	Asp	Val	
			-10					-5				-1	1		

35

TAC	CAC	GAC	GGT	GCC	TGT	CCC	GAA	GTC	AAG	CCA	GTC	GAC	AAC	TTC	135
Tyr	His	Asp	Gly	Ala	Cys	Pro	Glu	Val	Lys	Pro	Val	Asp	Asn	Phe	
		5					10					15			

40

GAC	TGG	TCC	CAG	TAC	CAT	GGT	AAA	TGG	TGG	CAG	GTC	GCC	GCG	TAC	180
Asp	Trp	Ser	Gln	Tyr	His	Gly	Lys	Trp	Trp	Gln	Val	Ala	Ala	Tyr	
		20					25					30			

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CCC	GAT	CAT	ATT	ACG	AAG	TAC	GGA	AAG	TGC	GGA	TGG	GCT	GAG	TAC	225
Pro	Asp	His	Ile	Thr	Lys	Tyr	Gly	Lys	Cys	Gly	Trp	Ala	Glu	Tyr	
		35					40					45			

	ACT	CCT	GAA	GGC	AAG	AGT	GTC	AAA	GTT	TCG	CGC	TAC	TCT	GTA	ATC	270
	Thr	Pro	Glu	Gly	Lys	Ser	Val	Lys	Val	Ser	Arg	Tyr	Ser	Val	Ile	
			50					55					60			
5	CAC	GGC	AAG	GAA	TAC	TTT	TCC	GAA	GGT	ACC	GCC	TAC	CCA	GTT	GGT	315
	His	Gly	Lys	Glu	Tyr	Phe	Ser	Glu	Gly	Thr	Ala	Tyr	Pro	Val	Gly	
			65					70					75			
10	GAC	TCC	AAG	ATT	GGA	AAG	ATC	TAC	CAC	AGC	TAC	ACT	ATT	GGA	GGT	360
	Asp	Ser	Lys	Ile	Gly	Lys	Ile	Tyr	His	Ser	Tyr	Thr	Ile	Gly	Gly	
			80					85					90			
15	GTG	ACC	CAG	GAG	GGT	GTA	TTC	AAC	GTA	CTC	TCC	ACT	GAC	AAC	AAG	405
	Val	Thr	Gln	Glu	Gly	Val	Phe	Asn	Val	Leu	Ser	Thr	Asp	Asn	Lys	
			95					100					105			
20	AAC	TAC	ATC	ATC	GGA	TAC	TTT	TGC	TCG	TAC	GAC	GAG	GAC	AAG	AAG	450
	Asn	Tyr	Ile	Ile	Gly	Tyr	Phe	Cys	Ser	Tyr	Asp	Glu	Asp	Lys	Lys	
			110					115					120			
25	GGA	CAC	ATG	GAC	TTG	GTC	TGG	GTG	CTC	TCC	AGA	AGC	ATG	GTC	CTT	495
	Gly	His	Met	Asp	Leu	Val	Trp	Val	Leu	Ser	Arg	Ser	Met	Val	Leu	
			125					130					135			
30	ACT	GGT	GAA	GCC	AAG	ACC	GCT	GTC	GAG	AAC	TAC	CTT	ATC	GGC	TCC	540
	Thr	Gly	Glu	Ala	Lys	Thr	Ala	Val	Glu	Asn	Tyr	Leu	Ile	Gly	Ser	
			140					145					150			
35	CCA	GTA	GTC	GAC	TCC	CAG	AAA	CTG	GTA	TAC	AGT	GAC	TTC	TCT	GAA	585
	Pro	Val	Val	Asp	Ser	Gln	Lys	Leu	Val	Tyr	Ser	Asp	Phe	Ser	Glu	
			155					160					165			
40	GCC	GCC	TGC	AAG	GTC	AAC	AAT	AGC	AAC	TGG	TCT	CAC	CCG	CAG	TTC	630
	Ala	Ala	Cys	Lys	Val	Asn	Asn	Ser	Asn	Trp	Ser	His	Pro	Gln	Phe	
			170					175					180			
45	GAA	AAA	GGT	GGC	GGC	GGT	GGT	ACA	CCA	GAA	ATG	CCT	GTT	CTG	GAA	675
	Glu	Lys	Gly	Gly	Gly	Gly	Gly	Thr	Pro	Glu	Met	Pro	Val	Leu	Glu	
			185					190					195			
50	AAC	CGG	GCT	GCT	CAG	GGC	GAT	ATT	ACT	GCA	CCC	GGC	GGT	GCT	CGC	720
	Asn	Arg	Ala	Ala	Gln	Gly	Asp	Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	
			200					205					210			
55	CGT	TTA	ACG	GGT	GAT	CAG	ACT	GCC	GCT	CTG	CGT	GAT	TCT	CTT	AGC	765
	Arg	Leu	Thr	Gly	Asp	Gln	Thr	Ala	Ala	Leu	Arg	Asp	Ser	Leu	Ser	
			215					220					225			
60	GAT	AAA	CCT	GCA	AAA	AAT	ATT	ATT	TTG	CTG	ATT	GGC	GAT	GGG	ATG	810
	Asp	Lys	Pro	Ala	Lys	Asn	Ile	Ile	Leu	Leu	Ile	Gly	Asp	Gly	Met	
			230					235					240			
65	GGG	GAC	TCG	GAA	ATT	ACT	GCC	GCA	CGT	AAT	TAT	GCC	GAA	GGT	GCG	855
	Gly	Asp	Ser	Glu	Ile	Thr	Ala	Ala	Arg	Asn	Tyr	Ala	Glu	Gly	Ala	
			245					250					255			
70	GGC	GGC	TTT	TTT	AAA	GGT	ATA	GAT	GCC	TTA	CCG	CTT	ACC	GGG	CAA	900
	Gly	Gly	Phe	Phe	Lys	Gly	Ile	Asp	Ala	Leu	Pro	Leu	Thr	Gly	Gln	
			260					265					270			

	TAC	ACT	CAC	TAT	GCG	CTG	AAT	AAA	AAA	ACC	GGC	AAA	CCG	GAC	TAC	945
	Tyr	Thr	His	Tyr	Ala	Leu	Asn	Lys	Lys	Thr	Gly	Lys	Pro	Asp	Tyr	
			275					280					285			
5	GTC	ACC	GAC	TCG	GCT	GCA	TCA	GCA	ACC	GCC	TGG	TCA	ACC	GGT	GTC	990
	Val	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Thr	Ala	Trp	Ser	Thr	Gly	Val	
			290					295					300			
10	AAA	ACC	TAT	AAC	GGC	GCG	CTG	GGC	GTC	GAT	ATT	CAC	GAA	AAA	GAT	1035
	Lys	Thr	Tyr	Asn	Gly	Ala	Leu	Gly	Val	Asp	Ile	His	Glu	Lys	Asp	
			305					310					315			
15	CAC	CCA	ACG	ATT	CTG	GAA	ATG	GCA	AAA	GCC	GCA	GGT	CTG	GCG	ACC	1080
	His	Pro	Thr	Ile	Leu	Glu	Met	Ala	Lys	Ala	Ala	Gly	Leu	Ala	Thr	
			320					325					330			
20	GGT	AAC	GTT	TCT	ACC	GCA	GAG	TTG	CAG	GAT	GCC	ACG	CCC	GCT	GCG	1125
	Gly	Asn	Val	Ser	Thr	Ala	Glu	Leu	Gln	Asp	Ala	Thr	Pro	Ala	Ala	
			335					340					345			
25	CTG	GTG	GCA	CAT	GTG	ACC	TCG	CGC	AAA	TGC	TAC	GGT	CCG	AGC	GCG	1170
	Leu	Val	Ala	His	Val	Thr	Ser	Arg	Lys	Cys	Tyr	Gly	Pro	Ser	Ala	
			350					355					360			
30	ACC	AGT	GAA	AAA	TGT	CCG	GGT	AAC	GCT	CTG	GAA	AAA	GGC	GGA	AAA	1215
	Thr	Ser	Glu	Lys	Cys	Pro	Gly	Asn	Ala	Leu	Glu	Lys	Gly	Gly	Lys	
			365					370					375			
35	GGA	TCG	ATT	ACC	GAA	CAG	CTG	CTT	AAC	GCT	CGT	GCC	GAC	GTT	ACG	1260
	Gly	Ser	Ile	Thr	Glu	Gln	Leu	Leu	Asn	Ala	Arg	Ala	Asp	Val	Thr	
			380					385					390			
40	CTT	GGC	GGC	GGC	GCA	AAA	ACC	TTT	GCT	GAA	ACG	GCA	ACC	GCT	GGT	1305
	Leu	Gly	Gly	Gly	Ala	Lys	Thr	Phe	Ala	Glu	Thr	Ala	Thr	Ala	Gly	
			395					400					405			
45	GAA	TGG	CAG	GGA	AAA	ACG	CTG	CGT	GAA	CAG	GCA	CAG	GCG	CGT	GGT	1350
	Glu	Trp	Gln	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	
			410					415					420			
50	TAT	CAG	TTG	GTG	AGC	GAT	GCT	GCC	TCA	CTG	AAT	TCG	GTG	ACG	GAA	1395
	Tyr	Gln	Leu	Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	
			425					430					435			
55	GCG	AAT	CAG	CAA	AAA	CCC	CTG	CTT	GGC	CTG	TTT	GCT	GAC	GGC	AAT	1440
	Ala	Asn	Gln	Gln	Lys	Pro	Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	
			440					445					450			
60	ATG	CCA	GTG	CGC	TGG	CTA	GGA	CCG	AAA	GCA	ACG	TAC	CAT	GGC	AAT	1485
	Met	Pro	Val	Arg	Trp	Leu	Gly	Pro	Lys	Ala	Thr	Tyr	His	Gly	Asn	
			455					460					465			
65	ATC	GAT	AAG	CCC	GCA	GTC	ACC	TGT	ACG	CCA	AAT	CCG	CAA	CGT	AAT	1530
	Ile	Asp	Lys	Pro	Ala	Val	Thr	Cys	Thr	Pro	Asn	Pro	Gln	Arg	Asn	
			470					475					480			
70	GAC	AGT	GTA	CCA	ACC	CTG	GCG	CAG	ATG	ACC	GAC	AAA	GCC	ATT	GAA	1575
	Asp	Ser	Val	Pro	Thr	Leu	Ala	Gln	Met	Thr	Asp	Lys	Ala	Ile	Glu	
			485					490					495			

